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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Gapop 10.0 , Gapext 0.5
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375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                               sp_archea:*
sp_bacteria:*
sp_fungi:*
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sp_rodent:*
sp_virus:*
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sp_phage:*
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sp_mhc:*
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sp_invertebrate:*
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sp_unclassified:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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75 75	76 75.5	77.5	78	80	90	84.5	84.5	95	116.5	124	339	353	375	Score
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	P91419 caenorhabdi Q9u2k1 caenorhabdi	Q9txh4 caenorhabdi Q9s709 arabidopsis	Q9nua2 homo sapien Q22873 caenorhabdi	09sbe6 zea mays su	Q9kmz5 vidio choi O81251 zea mavs su	024754 drosophila			-	Q9sew4 juglans reg	Q9spl5 macadamia i	Q9spl4 macadamia i	Q9spl3 macadamia i	Description

RESULT

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## ALIGNMENTS

Qy 1 KRDPQQREYEDCRRHCEQQEPR	Query Match 100.0%; Best Local Similarity 100.0%; Matches 66; Conservative (		DR PFAM; PF00546; Seedstore_7s; FT NON TER 1	INTER	HSSP; P02853; 2PHL.	RL Plant J. 0:0-0(1999).				RN [1]		OS MACADAMIA integrifolia (Macadamia nut). OC Fukarvota: Viridinlantae: Embryophyta: Tracheophyta:	AMP2	VICILIN PREC	DT 01-MAI-2000 (TEMBLIET 15, DT 01-OCT-2000 (TEMBLIET 15,	01-MAY-2000	Q9SPL3 PRELIMINARY;
KRDPOQREYEDCRRHCEQQEPRLOYQCQRRCOEQOROHGRGGDLMNPQRGGSGRYEEGEE 60	; Score 375; DB 10; Length 625; ; Pred. No. 1.2e-36; 0; Mismatches 0; Indels 0; Gaps	W; 415808A89D370296 CRC64;	1.			•	•	"A family of antimicrobial peptides is produced by processing of a 7S	Managara		ns; Proteaceae; Macadamia.				Last annotation update)	Crea	PRT; 625 AA.

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Tracheophyta; Sidicots; Rosidae;

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Best Local :
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EMBL; AF161884; AAD54245.1; -.
HSSP; P02853; 2PHL.
INTERPRO; IPPAGATOR.
                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE=NUT KERNEL;
Marcus J.P., Goulter K.C., Green
"A family of antimicrobial pepti
globulin protein in Macadamia ir
plant J. 0:0-0(1999)
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Eukaryota; Viridiplantae; Embryophyta; Tra
Magnoliophyta; eudicotyledons; Proteaceae;
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01-OCT-2000
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Marcus J.P., Goulter K.C.,
"A family of antimicrobial
"A family of antimicrobial
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Magnoliophyta; eudicotyledons; Proteaceae; Macadamia
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   KRDPQQREYEDCRRHCEQQEPRLQYQCQRRCQEQQRQHGRGGDLMNPQRGGSGRYEEGEE
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                                                                   1 Similarity
59; Conserv
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peptides is
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                                                                                                                                                  C752B884B2DF0224 CRC64;
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01-NOV-1996 (TrEMBLrel. (
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01-CT-2000 (TrEMBLrel. 1
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Q9SEW4;
01-MAY-2000
01-MAY-2000
01-OCT-2000
McHenry L., Fritz P.J.;

"Comparison of the structure and nucleotide sequences of vicilin of cocca and cotton raise questions about vicilin evolution."; plant Mol. Biol. 18:1173-1176(1992).

EMBL; X62625; CAA44493.1; -.

EMBL; X6266; CAA44494.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-CV. SUNLAND; TISSUE-SOMATIC EMBRYO LINE; Teuber S.S., Jarvis K.C., Peterson W.R., Dandekar A.M., "Identification and cloning of a cDNA encoding a vicili Jug r 2, from English wainut kernel (Juglans regia): a allergen.";
                                                                                                                                                                                              Theobroma cacao (Cacao).

Eukaryota; Viridiplantae; Embr

Bugaroliophyta; eudicotyledons;

Malvales; Malvaceae; Theobroma
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                                                                                                               TISSUE=LEAVES;
MEDLINE=92288309; PubMed=1600151;
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                                                                                                                                                                             NCBI_TaxID=3641;
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                                                                                                                                                                                                Theobroma
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01,
15,
                                                                                                                                                                                                                            Embryophyta; Tracheophyta;
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Pred. No. 6.8e
12; Mismatches
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Last annotation update)
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                                                                                                                                                                                                               eudicots;
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DB 10; .8e-07;

Length

593;

20;

Indels

8

Gaps

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525

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Rosidae;

Spermatophyta;

eurosids

genes

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RESULT

003678

ID 3678

ID 27

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DT 01

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                             RESULT
Q9ZWI3
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Best Local S
Matches 20
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Best Local S
Matches 25
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01-NOV-1996 (TrEMBLrel. 0
01-NOV-1996 (TrEMBLrel. 0
01-OCT-2000 (TrEMBLrel. 1
FETAL STORAGE PROTEIN.
Q9ZWI3;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Barley embryo globulin 1 gene, Beg1: characterization chromosome mapping and regulation of expression."; Mol. Gen. Genet. 239:209-218(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hordeum vulgare (Barley),
Eukaryota; Viridiplantae;
Magnoliophyta; Liliopsida;
                                                                                                                                                                                                                                                                                                 Seed storage protein.
SEQUENCE 637 AA; 72252 MW;
                                                                                                                                                                                                                                                                                                                                PROSITE; PS00867; CPSASE_2; UNKNOWN_1. PRODOM; PD081059; -; 1.
                                                                                                                                                                                                                                                                                                                                                               PFAM; PF00546; Seedstore_7s;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=93287988; PubMed=8510647;
Heck G.R., Chamberlain A.C., Ho T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                            INTERPRO; IPR000901;
INTERPRO; IPR001113;
                                                                                                                                                                                                                                                                                                                                                                                                            MENDEL; 8553; Horvu;1188;8553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4513,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRODOM; PD081059;
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PFAM; PF00546; Seeds
                                                                                             102 RHGEGEREE 110
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                                                                                                                                                        QQCVQRCRQERPRYSHARCVQECRDDQQQHGRHEQEEEQGRGRGWHGEGEREEEHGRGRG 101
                                                                                                                                                                                      EDCRRHCEQQEPRLQY-QCQRRCQEQQRQHGRGGDLMNPQRG-------
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M81719; AAA34269.1;
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20; Conser
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25; Conserv
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525 AA;
              PRELIMINARY;
                                                                                                                                                                                                                       Conservative
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525
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39.7%;
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01, Last sequence update)
15, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and Triticum aestivum (Wheat).
Embryophyta; Tracheophyta; Spermatophyta;
; Poales; Poaceae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
                                                                                                                                                                                                                    Score 95; DB
Pred. No. 0.00
12; Mismatches
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Pred. No. 4.
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              PRT;
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NO. 4.7e-06;
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                                                                                                                                                                                      ----GSG 53
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RESULT
Q24754
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Eukaryota; Metazo
Pterygota; Neopte
Ephydroidea; Dros
NCBI_TaxID=7244;
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Q24754;
01-NOV-1996
01-NOV-1996
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01-MAY-1999
01-OCT-2000
PV100.
                                                 SEQUENCE FROM N.A.
MEDLINE=94355848; PubMed=8083889;
Newfeld S.J., Tachida H., Yedvobn
"Drive-selection equilibrium: hom
gene mastermind.";
                                                                                                                                                             Newfeld S.J., Schmid A.T., Yedvobnick B.; "Homopolymer length variation in the Dros J. Mol. Evol. 37:483-495(1993).
                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 260-762 FROM N.A. MEDLINE-91251140; PubMed=1904096; Newfeld S.J., Smoller D.A., Yedvo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yamada K., Shimada T., Kondo M., Nishimura M., Hara-Nishimura I "Multiple functional proteins are produced by cleaving Asn-Gln of a single precursor by vacuolar processing enzyme."; J. Biol. Chem. 274:2563-2570(1999).
EEMBL; AB019195; BAA34056.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Embryophyta; Trachec Magnoliophyta; eudicotyledons; core eudicots; Cucurbitales; Cucurbitaceae; Cucurbita.
                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=941111143; PubMed=8283480;
SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cucurbita maxima (Pumpkin) (Winter squash). Eukaryota; Viridiplantae; Embryophyta; Trac
                                                                                                                                                                                                                                                                                         mastermind.
                                                                                                                                                                                                                                                                                                            "Interspecific comparison
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                                                                                                                                                                                                                                                                                                                                                                                                                     virilis (Fruit fly).

Metazoa; Arthropoda; Tracheata; Hexapoda; Tnsecta;
Neoptera; Endopterygota; Diptera; Brachy. . Musc
a; Drosophilidae; Drosophila.
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(TrembLrel. 10, Last seq
(TrembLrel. 15, Last ann
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                                      38:637-641(1994)
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                                                                                         Yedvobnick B.;
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Last annotation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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Pred. No. 0.04
19; Mismatches
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Last annotation update)
                                                                      homopolymer evolution
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unusually
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Best Local
                                                                       081251 PRELIMINARY;
081251;
01-NOV-1998 (TrEMBLrel. 0
01-NOV-1998 (TrEMBLrel. 0
01-OCT-2000 (TrEMBLrel. 1
GLOBULIN-1 (FRAGMENT).
Zea mays subsp. mays (maize).
Zea mays subsp. mays (maize).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
NCBI_TaxID=4578;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

SEROTYPE 01;

MEDLINE=2040683; PubMed=10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Dodson R.J., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Dragoi I., Sellers P.,

Gill S.R., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,

McDonald S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Newfeld S.J.;
Submitted (MAY-1992) to the EMBL/GenBank/DDBJ databases.
EMBL; M92914; AAC37201.1; -.
FLYBASE; FB9n0013119; Dvir\mam.
SEQUENCE 1655 AA; 175048 MW; 247D8F8DF0DDDE12 CRC64.
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE004357; AAF96084.1; -. TIGR; VCA0171; -.
                                                                                                                                                                                                                                                                                                                                                                                                               "DNA sequence of both chromosomes cholerae.";
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                                                                                                                                                                                                                                                                                                                                                                                                   Nature 406:477-483(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=666;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL PROTEIN VCA0171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma
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19; Conser
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28.8%;
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Last annotation updat
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Pred. No. 0.08
13; Mismatches
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Pred. No. 0.09
18; Mismatches
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RESULT
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Q9SBE6;
Q9SBE6;
01-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-OCT-2000 (TrEMBLrel. 1
Q9NUA2;
Q9NUA2;
Q1-QCT-2000
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HSSP; P50477; 1CAU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Speciation and domestication in maize evidence from the Globulin-1 gene."; Genetics 0:0-0(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zea mays subsp. parviglumis.
Eukaryota; Viridiplantae; Embryophyta; Trac
Magnoliophyta; Liliopsida; Poales; Poaceae;
NCBI_TaxID-76912;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        evidence from the Globulin-1 gene. Genetics 0:0-0(1998).
EMBL; AF064214; AAC31457.1; -.
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PROSITE; PS00867; CPSASE_2; UNKNOWN_1
NON_TER 242 242
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PFAM; PF00546; Seeds
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MENDEL; 31893; Zeama;1188;31893.
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27856 MW;
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Pred. No.
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ceae; Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gruidl M.E.,
Strome S., B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation updat
ATP-DEPENDENT RNA HELICASE GLH-1.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-BRISTOL N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUL-1996) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity
18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66
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                                                                                                                                                                                                         IPR001650; -.
IPR001878; -.
0098; zf-CCHC; 4.
                                                                                                                                                                                                                                                                            IPR001410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ., Smith P.A., Bennett K.L.;
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539 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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CAB87955.1;
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55444 MW;
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Score
Pred.
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Pred. No. 0.
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Catarrhini; Hominidae; Homo
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                                                                                  FD5A53BCA8F9355E CRC64;
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DB 5;
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Best Local Similarity
Matches 22; Conser
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Q9S709;
01-MAY-2000
01-MAY-2000
01-JUN-2000
T22C5.10.
T17H3.14.
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Q9TXH4;
01-MAY-2000
01-MAY-2000
01-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Roussell D.L., McCrone J.S., Smith P.A., Gruidl M.E., Submitted (JUL-1998) to the EMBL/GenBank/DDBJ database EMBL; L19948; AAC27384.1; -. INTERPRO; IPR000629; -. INTERPRO; IPR001410; -. INTERPRO; IPR001550; -. INTERPRO; IPR001678; -. INTERPRO; IPR001678; -. INTERPRO; IPR001678; -. INTERPRO; IPR001978; -. INTERPRO; IP
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM; PF00271; helicase_C; PRINTS; PR01228; EGGSHELL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad.
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "glh-1, a germ-line putative RNA helicase from Caenorhabditis, four zinc fingers.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=94022363; PubMed=8415696;
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                                                          (TrEMBLrel.
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 14, Last annotation update)
                                                                                                  (TrEMBLrel.
                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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Pred. No. 0.
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RA VYSOLSKAIA V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,

RA Lee J.M., Liu A., Li J., Gonzalez A., Liu K., Vaysberg M., Sakano H.,

RA Lee J.M., Liu A., Li J., Gonzalez A., Liu K., Vaysberg M., Sakano H.,

RA Chin C., Howng B., Choi E., Chiou J., Altafi H., Araujo R., Brooks S.,

RA Buehler E., Chao Q., Conn L., Conway A.B., Dunn P., Hansen N.,

RA Huizar L., Khan S., Kim C., Palm C., Robey D., Shinn P., Walker M.,

RA Davis R.W., Ecker J. R., Federspiel N.A., Theologis A.;

"Arabidopsis thaliana chromosome 1 BAC T17H3 sequence.";

RI Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AC012375; AAR24943 1: -.

DR EMBL; AC012375; AAR24943 1: -.

DR INTERPRO; IPR000574; -.

DR INTERPRO; IPR000571; -.

DR PFAM; PF00076; rrm; 1.

DR PFAM; PF00076; zf-CCH; 2.

SQ SEQUENCE 296 AA; 34572 MW; F284D29BF68445BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                       Matches 21; Conservative
                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C., Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C., Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu S., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A., Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases. [2]
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                                                                                                                                                                                          215 RRDPSHREFSHRDRDREFYRHGSGKRSSERSERQERDGSRGRRQASPKRGGSPGGGREGS 274
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                                                                                                                                                  60 EKQ 62
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                                                                                                         EER 277
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Pred. No. 0.11;
9; Mismatches 32;
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